

Minnifield
10/789536

10/789536

L1 FILE 'REGISTRY' ENTERED AT 12:10:19 ON 21 JAN 2005
157 S GGGGTCAACGTTTCAGGGGGG | GCATGACGTTGAGCT/SQSN

L2 FILE 'CAPLUS' ENTERED AT 12:12:01 ON 21 JAN 2005
55 S L1

L8 21 SEA ABB=ON PLU=ON L2(L) (IMMUNOMODULAT? OR IMMUNOSTIMULAT? OR
IMMUNOSTIMULANT OR IMMUNORESPONS? OR (IMMUN# OR IMMUNOL?) (3A) (M
ODULAT? OR STIMULAT? OR STIMULANT OR RESPONS?))

E1 THROUGH E29 ASSIGNED

Searcher : Shears 571-272-2528

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 19, 2005, 01:27:37 ; Search time 588 Seconds
(without alignments)
1608.493 Million cell updates/sec

Title: US-10-789-536-1
Perfect score: 20
Sequence: 1 GGGGTCACGTCACG99999 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapect 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pac:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 6 AR096686	AR096686 Sequence
2	20	100.0	20 6 AR135030	AR135030 Sequence
3	20	100.0	20 6 AX342378	AX342378 Sequence
4	20	100.0	20 6 AX342405	AX342405 Sequence
5	20	100.0	20 6 AX342438	AX342438 Sequence
6	18.4	92.0	20 6 AR140453	AR140453 Sequence
7	18.4	92.0	20 6 AR154761	AR154761 Sequence
8	18.4	92.0	20 6 BD190419	BD190419 Microemul
9	18.4	92.0	20 6 AR182880	AR182880 Sequence
10	18.4	92.0	20 6 AR182887	AR182887 Sequence
11	18.4	92.0	20 6 AR222213	AR222213 Sequence
12	18.4	92.0	20 6 AR432435	AR432435 Sequence
13	18.4	92.0	20 6 AX063578	AX063578 Sequence
14	18.4	92.0	20 6 AX088932	AX088932 Sequence
15	18.4	92.0	20 6 AX104327	AX104327 Sequence
16	18.4	92.0	20 6 AX104575	AX104575 Sequence
17	18.4	92.0	20 6 AX104776	AX104776 Sequence
18	18.4	92.0	20 6 AX104777	AX104777 Sequence
19	18.4	92.0	20 6	AX104777 Sequence

20	18.4	92.0	20 6 AX105103	AX105103 Sequence
21	18.4	92.0	20 6 AX105236	AX105236 Sequence
22	18.4	92.0	20 6 AX135634	AX135634 Sequence
23	18.4	92.0	20 6 AX194489	AX194489 Sequence
24	18.4	92.0	20 6 AX355408	AX355408 Sequence
25	18.4	92.0	20 6 AX355409	AX355409 Sequence
26	18.4	92.0	20 6 AX465439	AX465439 Sequence
27	18.4	92.0	20 6 AX468483	AX468483 Sequence
28	18.4	92.0	20 6 AX547380	AX547380 Sequence
29	18.4	92.0	20 6 AX547628	AX547628 Sequence
30	18.4	92.0	20 6 AX547829	AX547829 Sequence
31	18.4	92.0	20 6 AX547830	AX547830 Sequence
32	18.4	92.0	20 6 BD009060	BD009060 Immunobtl
33	18.4	92.0	20 6 BD069974	BD069974 Use of nu
34	18.4	92.0	21 6 AX104812	AX104812 Sequence
35	18.4	92.0	21 6 AX105257	AX105257 Sequence
36	18.4	92.0	21 6 AX547865	AX547865 Sequence
37	18.4	92.0	24 6 AX104326	AX104326 Sequence
38	18.4	92.0	24 6 AX547379	AX547379 Sequence
39	17.4	87.0	19 6 CO753472	CO753472 Sequence
40	17.4	87.0	19 6 CO753473	CO753473 Sequence
41	17.4	87.0	19 6 AX194446	AX194446 Sequence
42	17.4	87.0	19 6 AX465396	AX465396 Sequence
43	17.4	87.0	19 6 AX771751	AX771751 Sequence
44	17.4	87.0	19 6 AX771752	AX771752 Sequence
45	17.4	87.0	2 AC013515	AC013515 Homo sapi

ALIGNMENTS

RESULT 1

LOCUS AR096686 20 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 1 from patent US 6008200.

ACCESSION AR096686

VERSION AR096686.1 GI:10025701

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kriegl,A.M.

TITLE Immunomodulatory oligonucleotides

JOURNAL Patent: US 6008200-A 1-28-DEC-1999;

FEATURES

Location/Qualifiers

Source 1..20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCACGTCACG99999 20

Db 1 GGGGTCACGTCACG99999 20

RESULT 2

LOCUS AR135030 20 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 1 from patent US 6194388.

ACCESSION AR135030

VERSION AR135030.1 GI:14123935

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kriegl,A.M., Kliman,D. and Steinberg,A.D.

TITLE Immunomodulatory oligonucleotides

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 06:37:10 ; Search time 209.714 Seconds
(without alignments)
547.973 Million cell updates/sec

Title: US-10-789-536-1

Perfect score: 20
1 9999TCAAGTCAAG9999 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-09-415-142-1
2	20	100.0	20	10	US-09-931-583-1
3	20	100.0	20	16	US-10-631-676-1
4	20	100.0	20	17	US-10-789-051-1
5	20	100.0	20	17	US-10-690-495-1
6	20	100.0	20	17	US-10-788-191-1
7	20	100.0	20	17	US-10-789-536-1
8	20	100.0	20	17	US-10-789-536-1
9	20	100.0	20	17	US-10-789-533-1
10	20	100.0	20	17	US-10-787-737-1
11	20	100.0	20	17	US-10-788-199-1
12	20	100.0	20	18	US-10-847-650-1

13	18.4	92.0	20	10	US-09-888-326-436	Sequence 436, App
14	18.4	92.0	20	10	US-09-888-326-437	Sequence 437, App
15	18.4	92.0	20	10	US-09-818-918-12	Sequence 12, App1
16	18.4	92.0	20	10	US-09-776-479-519	Sequence 519, App
17	18.4	92.0	20	10	US-09-776-479-519	Sequence 767, App
18	18.4	92.0	20	10	US-09-776-479-968	Sequence 968, App
19	18.4	92.0	20	10	US-09-776-479-969	Sequence 969, App
20	18.4	92.0	20	10	US-09-967-664-3	Sequence 3, App1
21	18.4	92.0	20	11	US-09-776-479-519	Sequence 519, App
22	18.4	92.0	20	11	US-09-776-479-519	Sequence 767, App
23	18.4	92.0	20	11	US-09-776-479-968	Sequence 968, App
24	18.4	92.0	20	11	US-09-776-479-969	Sequence 969, App
25	18.4	92.0	20	11	US-09-965-101-52	Sequence 52, App1
26	18.4	92.0	20	11	US-09-965-101-59	Sequence 59, App1
27	18.4	92.0	20	14	US-10-112-653-496	Sequence 496, App
28	18.4	92.0	20	14	US-10-112-653-740	Sequence 740, App
29	18.4	92.0	20	14	US-10-112-653-923	Sequence 923, App
30	18.4	92.0	20	14	US-10-017-995-519	Sequence 519, App
31	18.4	92.0	20	14	US-10-017-995-767	Sequence 767, App
32	18.4	92.0	20	14	US-10-017-995-968	Sequence 968, App
33	18.4	92.0	20	14	US-10-017-995-969	Sequence 969, App
34	18.4	92.0	20	15	US-10-161-229-47	Sequence 47, App1
35	18.4	92.0	20	15	US-10-194-035-89	Sequence 89, App1
36	18.4	92.0	20	15	US-10-224-523-35	Sequence 35, App1
37	18.4	92.0	20	15	US-10-187-264-12	Sequence 12, App1
38	18.4	92.0	20	15	US-10-306-522-12	Sequence 12, App1
39	18.4	92.0	20	15	US-10-314-578-519	Sequence 519, App
40	18.4	92.0	20	15	US-10-314-578-767	Sequence 767, App
41	18.4	92.0	20	15	US-10-314-578-968	Sequence 968, App
42	18.4	92.0	20	15	US-10-314-578-969	Sequence 969, App
43	18.4	92.0	20	16	US-10-455-247-3	Sequence 3, App1
44	18.4	92.0	20	16	US-10-719-493-12	Sequence 12, App1
45	18.4	92.0	20	17	US-10-627-331-12	Sequence 12, App1

ALIGNMENTS

RESULT 1
US-09-415-142-1
Sequence 1, Application US/09415142
Publication No. US20030026782A1
GENERAL INFORMATION:
APPLICANT: Kline, Arthur M.
APPLICANT: Kline, Arthur M.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/09/415,142
CURRENT FILING DATE: 1999-10-09
PRIORITY APPLICATION NUMBER: US 08/386,063
PRIORITY FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-415-142-1

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACCTTCAGGCGG 20
Db 1 GGGGTCAACCTTCAGGCGG 20

RESULT 2
US-09-931-583-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:49:12 ; Search time 1626.29 Seconds
(without alignments)
448.134 Million cell updates/sec

Title: US-10-789-536-1

Perfect score: 20

Sequence: 1 999gtcaacgtcagcagcagcagc 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	92.0	414	5	BX678404 BX678404
C 2	18.4	92.0	558	5	BX253788 BX253788
C 3	17.4	87.0	281	1	AV294749 AV294749
C 4	17.4	87.0	437	1	AV772436 AV772436
C 5	17.4	87.0	692	9	CG143495 PUIH657B
C 6	17.4	87.0	708	2	BB629098 BB629098
C 7	17.4	87.0	721	8	AA414593 RPT-11-1
C 8	17.4	87.0	884	8	BH950547 cd113c04
C 9	16.8	84.0	223	7	CF398170 RPTd3_21
C 10	16.8	84.0	243	7	BE643702 NCX1_043
C 11	16.8	84.0	336	2	BB532888 BB532888
C 12	16.8	84.0	341	2	AM888010 NXNV_105
C 13	16.8	84.0	361	2	BF516817 NXSI_003
C 14	16.8	84.0	381	5	BQ701308 NXSI_062
C 15	16.8	84.0	388	5	BX678528 BX678528
C 16	16.8	84.0	395	2	AM289674 AM289674
C 17	16.8	84.0	395	6	CD028242 NXNV004A0
C 18	16.8	84.0	451	2	BE431401 NXNV_181
C 19	16.8	84.0	477	5	BQ655830 NXRV099_H
C 20	16.8	84.0	491	5	BQ700582 NXSI_130
C 21	16.8	84.0	492	5	BQ700582 NXRV108_B
C 22	16.8	84.0	495	7	CF392169 RTDR3_8_B
C 23	16.8	84.0	505	1	AI813183 23H_Pine
C 24	16.8	84.0	505	2	AM985091 NXNV_130

C 25	16.8	84.0	512	2	BF517774 BF517774
C 26	16.8	84.0	530	6	CA354197 CA354197
C 27	16.8	84.0	532	4	BQ75515 NXSI_139
C 28	16.8	84.0	546	1	AA556997 839_Lobio
C 29	16.8	84.0	561	7	CF673102 RTCN1_76
C 30	16.8	84.0	566	7	CF476621 RTMW3_2D
C 31	16.8	84.0	598	7	CF392026 RTDR3_12
C 32	16.8	84.0	626	1	AL751023 AL751023
C 33	16.8	84.0	626	1	AA557077 AA557077
C 34	16.8	84.0	634	5	BX253042 BX253042
C 35	16.8	84.0	641	5	BX784262 BX784262
C 36	16.8	84.0	648	7	CF389798 RTDR2_5E
C 37	16.8	84.0	653	5	BQ633853 BQ633853
C 38	16.8	84.0	660	7	CF401770 RTMW1_14
C 39	16.8	84.0	662	7	CF386290 RTDR1_13
C 40	16.8	84.0	662	7	CF390498 RTDR2_19
C 41	16.8	84.0	666	7	CO199154 CO199154
C 42	16.8	84.0	676	7	CF670509 RTCN1_50
C 43	16.8	84.0	691	7	CF473420 RTMW2_2A
C 44	16.8	84.0	694	7	CO174200 CO174200
C 45	16.8	84.0	700	8	AO888815 HS_3144_A

ALIGNMENTS

RESULT 1
BX678404/c BX678404 414 bp mRNA linear EST 28-OCT-2003
DEFINITION BX678404 RS Pinus pinaster cDNA clone RS08F09, mRNA sequence.
ACCESSION BX678404
VERSION BX678404.1 GI:38012342
KEYWORDS EST.

SOURCE
ORGANISM

Pinus pinaster
Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE

1 (bases 1 to 414)
Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
Unpublished (2002)

AUTHORS

TITLE

JOURNAL

COMMENT

Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: frigerio@piereton.inra.fr
Email: frigerio@piereton.inra.fr
Seq primer: T3.

FEATURES
source

Location/Qualifiers
1..414
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS08F09"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dr primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a phagescript phagemid."

ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 414;
Best Local Similarity 95.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 01:27:37 ; Search time 441 Seconds
(without alignments)
1608.493 Million cell updates/sec

Title: US-10-789-536-6

Sequence: 1 gcatacgttgagct 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb ba:*
2: gb hg:*
3: gb in:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb ph:*
8: gb pl:*
9: gb pr:*
10: gb ro:*
11: gb sts:*
12: gb sy:*
13: gb un:*
14: gb vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	6 AR096691	AR096691 Sequence
2	15	100.0	15	6 AR135035	AR135035 Sequence
3	15	100.0	15	6 AR140447	AR140447 Sequence
4	15	100.0	15	6 AR140457	AR140457 Sequence
5	15	100.0	15	6 AR140489	AR140489 Sequence
6	15	100.0	15	6 AR146293	AR146293 Sequence
7	15	100.0	15	6 AR146329	AR146329 Sequence
8	15	100.0	15	6 AR154677	AR154677 Sequence
9	15	100.0	15	6 BD205515	BD205515 Sequence
10	15	100.0	15	6 BD205551	BD205551 Method of
11	15	100.0	15	6 BD261057	BD261057 Method of
12	15	100.0	15	6 BD261093	BD261093 Method a
13	15	100.0	15	6 BD261226	BD261226 Method a
14	15	100.0	15	6 BD267831	BD267831 Method a
15	15	100.0	15	6 BD267861	BD267861 Method f
16	15	100.0	15	6 BD270732	BD270732 Stereoiso
17	15	100.0	15	6 AR213813	AR213813 Sequence
18	15	100.0	15	6 AR222180	AR222180 Sequence
19	15	100.0	15	6 AR433429	AR433429 Sequence

20	15	100.0	15	6 AX103874	AX103874 Sequence
21	15	100.0	15	6 AX103894	AX103894 Sequence
22	15	100.0	15	6 AX104574	AX104574 Sequence
23	15	100.0	15	6 AX104591	AX104591 Sequence
24	15	100.0	15	6 AX104643	AX104643 Sequence
25	15	100.0	15	6 AX105164	AX105164 Sequence
26	15	100.0	15	6 AX105184	AX105184 Sequence
27	15	100.0	15	6 AX105184	AX105184 Sequence
28	15	100.0	15	6 AX342410	AX342410 Sequence
29	15	100.0	15	6 AX342443	AX342443 Sequence
30	15	100.0	15	6 AX351733	AX351733 Sequence
31	15	100.0	15	6 AX351799	AX351799 Sequence
32	15	100.0	15	6 AX351820	AX351820 Sequence
33	15	100.0	15	6 AX351844	AX351844 Sequence
34	15	100.0	15	6 AX351871	AX351871 Sequence
35	15	100.0	15	6 AX352112	AX352112 Sequence
36	15	100.0	15	6 AX352131	AX352131 Sequence
37	15	100.0	15	6 AX355037	AX355037 Sequence
38	15	100.0	15	6 AX355291	AX355291 Sequence
39	15	100.0	15	6 AX355292	AX355292 Sequence
40	15	100.0	15	6 AX355293	AX355293 Sequence
41	15	100.0	15	6 AX355294	AX355294 Sequence
42	15	100.0	15	6 AX455576	AX455576 Sequence
43	15	100.0	15	6 AX546927	AX546927 Sequence
44	15	100.0	15	6 AX546947	AX546947 Sequence
45	15	100.0	15	6 AX547627	AX547627 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR096691 15 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6008200.
ACCESSION AR096691
VERSION AR096691.1 GI:10025709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Kriegl,A.M.
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: US 6008200-A 6 28-DEC-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GCATGACGTTGAGCT 15
Db 1 GCATGACGTTGAGCT 15

RESULT 2
LOCUS AR135035 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6194388.
ACCESSION AR135035
VERSION AR135035.1 GI:14123940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Kriegl,A.M.; Klitman,D. and Steinberg,A.D.
TITLE Immunomodulatory oligonucleotides

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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:57:22 | Search time 36 Seconds
(without alignments)

296.162 Million cell updates/sec

Title: US-10-789-536-6

Sequence: 1 gcacgacgtgagct 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	15	100.0	15	US-08-386-063-6	Sequence 6, Appli
3	15	100.0	15	US-08-738-652-6	Sequence 16, Appli
4	15	100.0	15	US-08-738-652-16	Sequence 16, Appli
5	15	100.0	15	US-08-738-652-48	Sequence 35, Appli
6	15	100.0	15	US-09-030-701-35	Sequence 5, Appli
7	15	100.0	15	US-09-286-098-5	Sequence 41, Appli
8	15	100.0	15	US-09-286-098-41	Sequence 6, Appli
9	15	100.0	15	US-08-960-774-6	Sequence 5, Appli
10	15	100.0	15	US-09-325-193A-5	Sequence 5, Appli
11	15	100.0	15	US-09-191-170-5	Sequence 6, Appli
12	15	100.0	15	US-09-337-619-6	Sequence 1548, Ap
13	15	89.3	519	US-09-543-681A-1544	Sequence 1598, Ap
14	15	89.3	532	US-09-543-681A-1598	Sequence 261, App
15	15	89.3	999	US-09-489-039A-90	Sequence 261, App
16	15	89.3	1001	US-09-641-638-261	Sequence 1840, Ap
17	15	89.3	1001	US-10-170-097-261	Sequence 33, Appli
18	15	89.3	1842	US-09-543-681A-1840	Sequence 675, App
19	15	89.3	1896	US-08-426-630-33	Sequence 3, Appli
20	15	89.3	2955	US-09-620-312D-675	Sequence 3, Appli
21	15	89.3	3039	US-09-620-312D-675	Sequence 3, Appli
22	15	89.3	3808	US-08-972-631-3	Sequence 3, Appli
23	15	89.3	3808	US-08-972-631-3	Sequence 3, Appli
24	15	89.3	3808	US-08-972-631-3	Sequence 3, Appli
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26	15	89.3	3808	US-08-972-631-3	Sequence 3, Appli
27	15	89.3	3808	US-09-225-170-3	Sequence 3, Appli

c	28	13.4	89.3	4748	4	US-08-426-630-29	Sequence 29, Appli
c	29	13.4	89.3	6045	4	US-09-091-501B-7	Sequence 7, Appli
c	30	13.4	89.3	10320	4	US-09-091-501B-9	Sequence 9, Appli
c	31	13.4	89.3	111282	3	US-09-754-250-3	Sequence 3, Appli
c	32	13	86.7	343	3	US-08-349-403-7	Sequence 7, Appli
c	33	13	86.7	508	4	US-09-248-796A-3977	Sequence 3977, Ap
c	34	13	86.7	1179	4	US-09-489-039A-2302	Sequence 2302, Ap
c	35	13	86.7	1551	1	US-09-603-787A-185	Sequence 185, App
c	36	13	86.7	1551	1	US-08-457-274A-1	Sequence 1, Appli
c	37	13	86.7	1551	1	US-08-457-274A-27	Sequence 27, Appli
c	38	13	86.7	1551	5	PCT-US95-05758-1	Sequence 1, Appli
c	39	13	86.7	1551	5	PCT-US95-05758-27	Sequence 27, Appli
c	40	13	86.7	2046	4	US-09-489-039A-4692	Sequence 4692, Ap
c	41	13	86.7	2085	1	US-08-457-274A-29	Sequence 29, Appli
c	42	13	86.7	2085	5	PCT-US95-05758-29	Sequence 29, Appli
c	43	13	86.7	2435	4	US-09-634-238-131	Sequence 131, App
c	44	13	86.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	45	13	86.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-386-063-6
Sequence 6, Application US/08386063
Patent No. 6008200
GENERAL INFORMATION:
APPLICANT: Arthur M. Krieg, M.D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,063
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ARNOLD, BETH E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIZ-013CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-386-063-6

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GCATGACGTGAGCT 15
Db 1 GCATGACGTGAGCT 15
RESULT 2

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OW nucleic - nucleic search, using sw model

Run on: January 19, 2005, 06:37:10 / Search time 157.286 Seconds
(without alignments)
547.973 Million cell updates/sec

Title: US-10-789-536-6

Perfect score: 15

Sequence: 1 gcacgacgtgagct 15

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications_NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	15	9	US-09-824-468-5
2	15	100.0	15	9	US-09-824-468-41
3	15	100.0	15	9	US-09-800-265A-5
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5	15	100.0	15	9	US-09-920-313-5
6	15	100.0	15	10	US-09-415-142-6
7	15	100.0	15	10	US-09-888-326-65
8	15	100.0	15	10	US-09-888-326-319
9	15	100.0	15	10	US-09-888-326-320
10	15	100.0	15	10	US-09-888-326-321
11	15	100.0	15	10	US-09-888-326-322
12	15	100.0	15	10	US-09-818-918-6

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14	15	100.0	15	10	US-09-818-918-48	Sequence 48, App1
15	15	100.0	15	10	US-09-931-583-6	Sequence 6, App1
16	15	100.0	15	10	US-09-776-479-66	Sequence 86, App1
17	15	100.0	15	10	US-09-776-479-86	Sequence 86, App1
18	15	100.0	15	10	US-09-776-479-766	Sequence 766, App
19	15	100.0	15	10	US-09-776-479-783	Sequence 783, App
20	15	100.0	15	10	US-09-776-479-835	Sequence 835, App
21	15	100.0	15	10	US-09-954-887B-53	Sequence 53, App1
22	15	100.0	15	11	US-09-874-991C-29	Sequence 29, App1
23	15	100.0	15	11	US-09-874-991C-95	Sequence 95, App1
24	15	100.0	15	11	US-09-874-991C-116	Sequence 116, App
25	15	100.0	15	11	US-09-874-991C-140	Sequence 140, App
26	15	100.0	15	11	US-09-874-991C-167	Sequence 167, App
27	15	100.0	15	11	US-09-874-991C-188	Sequence 188, App
28	15	100.0	15	11	US-09-874-991C-408	Sequence 408, App
29	15	100.0	15	11	US-09-874-991C-427	Sequence 427, App
30	15	100.0	15	11	US-09-776-479-66	Sequence 66, App1
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32	15	100.0	15	11	US-09-776-479-766	Sequence 766, App
33	15	100.0	15	11	US-09-776-479-783	Sequence 783, App
34	15	100.0	15	11	US-09-776-479-835	Sequence 835, App
35	15	100.0	15	11	US-09-776-479-86	Sequence 86, App
36	15	100.0	15	14	US-10-023-909A-5	Sequence 85, App
37	15	100.0	15	14	US-10-112-653-60	Sequence 60, App1
38	15	100.0	15	14	US-10-112-653-80	Sequence 80, App1
39	15	100.0	15	14	US-10-112-653-83	Sequence 83, App1
40	15	100.0	15	14	US-10-112-653-739	Sequence 739, App
41	15	100.0	15	14	US-10-112-653-756	Sequence 756, App
42	15	100.0	15	14	US-10-017-995-86	Sequence 86, App
43	15	100.0	15	14	US-10-017-995-86	Sequence 86, App1
44	15	100.0	15	14	US-10-017-995-766	Sequence 766, App
45	15	100.0	15	14	US-10-017-995-783	Sequence 783, App

ALIGNMENTS

RESULT 1
US-09-824-468-5
Sequence 5, Application US/09824468
Patent No. US20020064515A1
GENERAL INFORMATION:
APPLICANT: Krieger, Arthur M.
APPLICANT: Weimer, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/824,468
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/286,098
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-824-468-5

Query Match 100.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATGACGTGAGCT 15
|||
Db 1 GCATGACGTGAGCT 15

RESULT 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:49:12 ; Search time 1219.71 Seconds
(without alignments)
448.134 Million cell updates/sec

Title: US-10-789-536-6

Sequence: 1 gcacgacgttcgagct 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3282875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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7: gb_esc6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	15	100.0	355	1	AA437702 AA437702
C 3	15	100.0	368	1	AJ494292 AJ494292
C 4	15	100.0	368	1	AJ494293 AJ494293
C 5	15	100.0	376	1	AJ494285 AJ494285
C 6	15	100.0	424	2	BM145624 BM145624
C 7	15	100.0	428	5	BM242018 BM242018
C 8	15	100.0	486	5	BP094747 BP094747
C 9	15	100.0	491	1	AJ495145 AJ495145
C 10	15	100.0	502	1	AV988927 AV988927
C 11	15	100.0	534	1	AV948910 AV948910
C 12	15	100.0	566	1	AV984785 AV984785
C 13	15	100.0	572	1	AV996055 AV996055
C 14	15	100.0	594	1	BM353563 BM353563
C 15	15	100.0	601	1	AV964482 AV964482
C 16	15	100.0	602	5	BM345567 BM345567
C 17	15	100.0	605	5	BM352814 BM352814
C 18	15	100.0	609	5	BM247380 BM247380
C 19	15	100.0	621	5	BM339646 BM339646
C 20	15	100.0	625	5	BM244959 BM244959
C 21	15	100.0	635	1	BM244394 BM244394
C 22	15	100.0	636	1	AV985099 AV985099
C 23	15	100.0	637	5	BU555032 BU555032
C 24	15	100.0	640	5	BM340838 BM340838

C 25	15	100.0	643	5	BM434148 BM434148
C 26	15	100.0	645	1	AV988282 AV988282
C 27	15	100.0	646	5	BM347242 BM347242
C 28	15	100.0	647	1	AV996231 AV996231
C 29	15	100.0	648	5	BM259692 BM259692
C 30	15	100.0	651	1	AV672198 AV672198
C 31	15	100.0	653	5	BM244852 BM244852
C 32	15	100.0	654	1	AV672377 AV672377
C 33	15	100.0	654	5	BM254503 BM254503
C 34	15	100.0	663	5	BU555036 BU555036
C 35	15	100.0	665	5	BM433399 BM433399
C 36	15	100.0	677	5	BM434636 BM434636
C 37	15	100.0	678	1	AV990599 AV990599
C 38	15	100.0	678	6	CA350833 CA350833
C 39	15	100.0	679	5	BM113437 BM113437
C 40	15	100.0	682	5	BM230554 BM230554
C 41	15	100.0	696	1	AV974313 AV974313
C 42	15	100.0	701	5	BM243655 BM243655
C 43	15	100.0	702	5	BM268555 BM268555
C 44	15	100.0	704	5	BM431183 BM431183
C 45	15	100.0	712	5	BM124438 BM124438

ALIGNMENTS

RESULT 1

LOCUS BM247469/c 153 bp mRNA linear EST 09-NOV-2002
DEFINITION BM247469 Nori Satoh unpublished cDNA library, tailbud embryo Clona
ACCESSION BM247469
VERSION BM247469.1 GI:24827387
KEYWORDS EST.

SOURCE

ORGANISM Clona intestinalis
Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Clona.

1 (bases 1 to 153)

AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE Expressed genes in Clona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

Source

1..153
location/Qualifiers
/organism="Clona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="clb074008"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lilo="Nori Satoh unpublished cDNA library, tailbud embryo"

ORIGIN

Query Match 100.0%; Score 15; DB 5; Length 153;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 GCATGACGTGAGCT 15
|||||
|||||

Db

62 GCATGACGTGAGCT 48
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|||||

RESULT 2

AA437702/c 355 bp mRNA linear EST 30-MAY-1997
LOCUS AA437702